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LncRNAs expression signatures of cadmium-induced malignant transformation of human bronchial epithelial cells revealed by microarray

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Background

Cadmium (Cd) and its compounds are well-known environmental carcinogens, but the mechanisms underlying the carcinogenesis are not entirely understood yet. Long non-coding RNAs (lncRNAs) are an important class of pervasive genes involved in a variety of biological functions. They are aberrantly expressed in many types of cancers. In this study, we described lncRNAs profiles in 35th passage of $CdCI_2$ malignant transformation cells(35th cell) and untransformed human bronchial epithelial cells(16HBE) by microarray.

Methodology/principal findings

With abundant and varied probes accounting 33,045 LncRNAs in our microarray, the number of lncRNAs that expressed at a certain level could be detected is 21409. From the data we found there were 369 lncRNAs were upregulated and 90 lncRNAs were downregulated (≥2.0fold-change, $P<0.05$) in 35th cells compared with 16HBE cells. Our data showed that upregulated lncRNAs were more common than downregulated ones. ENST00000477387, ENST00000394732, ENST00000485873, ENST00000497538, uc002odz.1, AK023660, NR_023938, BC019085 were evaluated by qPCR in 35th cells compared with 16HBE cells. The eigth lncRNAs were aberrantly expressed in 35th cells compared with matched 16HBE cells.

Conclusions/significance

Our study is the first one to determine genome-wide lncRNAs expression patterns in Cadmium-induced malignant transformation by microarray. The results displayed that clusters of lncRNAs were aberrantly expressed in $CdCI_2$ malignant transformation cells compared with 16HBE cells, which revealed that lncRNAs differentially expressed in $CdCI_2$ malignant transformation cells may exert a partial or key role in cadmium-induced cancers. Taken together, this study may provide a viable mechanism for cadmium-induced cancers.

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